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## DD4b5.3 Coding Sequence

Length 2563 bp

1 GGCAGGGCAGGTGGAGCTCGGAGCTGCTGCTCTGGTTCTTGTGGCCACCGTCGCT  
 1 R G Q V G A R S C C F W F S C G H R R C - 60  
 61 GTCCGGCTGCCCTGGGCTGCCAACAGACAAGGGCTGGGCCACAGCACCTCAGAACCGA  
 61 P A A L G C R T D K A W A T A P Q K P T - 120  
 121 CGCAGCTCGACGCAGGGCCGGCAGGAGGGTGGCGATCGCGTGTGGAGGGCGCCGCGC  
 121 Q L D A G A G R R V G D R V S E G A A R - 180  
 181 GGGCAGGCGGGCGGGCGCCAGAGGGGAAAGAGGCAGGGCGGGTCAGCCGCTGGCC  
 181 A G G R A P E G E R G G G G S A A G R - 240  
 241 GGGCCGGCGGGGAATGTCGATGCCGACGCGATGCCGCTGCCGGGTCAGGGAGGAGC  
 241 A G G G M S M P D A M P L P G V G E E L - 300  
 301 TGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGTACTCCTTCATGCCACCGTCACCA  
 301 K Q A K E I E D A E K Y S F M A T V T K - 360  
 361 AGGCGCCAAGAACAAATCCAGTTGCTGATGACATGCAGGAGTTCACCAAATTCCCCA  
 361 A P K K Q I Q F A D D M Q E F T K F P T - 420  
 421 CCAAAACTGCCGAAGATCTTGTCTCGCTCGATCTCACAGTCCTCCACTGACAGCTACA  
 421 K T G R R S L S R S I S Q S S T D S Y S - 480  
 481 GTTCAGCTGCATCCTACACAGATAGCTGATGATGAGGTTCTCCCCGAGAGAACAGC  
 481 S A A S Y T D S S D D E V S P R E K Q Q - 540  
 541 AAACCAACTCCAAGGGCAGCAATTCTGTGTGAAGAACATCAAGCAGGCAGAACATTG  
 541 T N S K G S S N F C V K N I K Q A E F G - 600  
 601 GACGCCGGGAGATTGAGATTGAGACATGTCTGCTGATTCACTCAGGAAAC  
 601 R R E I E I A E Q D M S A L I S L R K R - 660  
 661 GTGCTCAGGGGGAGAACGCCCTGGCTGGCTAAATAGTGGCTGTACACACATCACAG  
 661 A Q G E K P L A G A K I V G C T H I T A - 720  
 721 CCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGCTCAGTGGCTGGCTG  
 721 Q T A V L I E T L C A L G A Q C R W S A - 780  
 781 CTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCGAGCACTGGCTGGAGTTG  
 781 C N I Y S T Q N E V A A A L A E A G V A - 840  
 841 CAGTGGCTGGAGGGCAGTCAGAACAGATGACTCTGGTGGTATTGACCGCTGTG  
 841 V F A W K G E S E D D F W W C I D R C V - 900  
 901 TGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGAGACTTAACCCACT  
 901 N M D G W Q A N M I L D D G G D L T H W - 960

FIG. 1

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961 GGGTTTATAAGAAGTATCCAAACGTGTTAAGAAGATCCGAGGCATTGTGGAAGAGAGCG + 1020  
 V Y K K Y P N V F K K I R G I V E E S V -  
 1021 TGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCA + 1080  
 T G V H R L Y Q L S K A G K L C V P A M -  
 1081 TGAACGTCAATGATTCTGTTACCAACAGAAGTTGATAACTGTACTGCTGCCGAGAAT + 1140  
 N V N D S V T K Q K F D N L Y C C R E S -  
 1141 CCATTTGGATGGCCTGAAGAGGACACAGATGTGATGTTGGTGGAAACAAGTGGTGG + 1200  
 I L D G L K R T T D V M F G G K Q V V V -  
 1201 TGTGTGGCTATGGTAGGTAGGCAAGGGCTGCTGCTGCTCAAAGCTTGGAGCAA + 1260  
 C G Y G E V G K G C C A A L K A L G A I -  
 1261 TTGTCTACATTACCGAAATCGACCCCCATCTGTGCTCTGCAGGCCATGGATGGATGGTTCA + 1320  
 V Y I T E I D P I C A L Q A C M D G F R -  
 1321 GGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTGCACAGGAA + 1380  
 V V K L N E V I R Q V D V V I T C T G N -  
 1381 ATAAGAATGTAGTGACACGGGAGCACTGGATCCATGAAAAACAGTTGATCGTATGCA + 1440  
 K N V V T R E H L D R M K N S C I V C N -  
 1441 ATATGGGCCACTCCAACACAGAAATCGATGTGACCAGGCCCTCCGACTCCGGAGCTGACGT + 1500  
 M G H S N T E I D V T S L R T P E L T W -  
 1501 GGGAGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCC + 1560  
 E R V R S Q V D H V I W P D G K R V V L -  
 1561 TCCTGGCAGAGGGTCGCTACTCAATTGAGCTGCTCCACAGTCCCACCTTGTTCGT + 1620  
 L A E G R L L N L S C S T V P T F V L S -  
 1621 CCATCACAGGCCACAACACAGGTTGGCACTGATAGAACTCTATAATGCACCCGAGGGC + 1680  
 I T A T T Q A L A L I E L Y N A P E G R -  
 1681 GATACAAGCAGGATGTGACTTGCTTCTAAGAAAATGGATGAATACGTTGCCAGCTGC + 1740  
 Y K Q D V Y L L P K K M D E Y V A S L H -  
 1741 ATCTGCCATCATTGATGCCACCTACAGAGCTGACAGATGACCAAGCAAATATCTGG + 1800  
 L P S F D A H L T E L T D D Q A K Y L G -  
 1801 GACTCAACAAAATGGGCATTCAAACCTAATTATTACAGATACTAATGGACCATACTAC + 1860  
 L N K N G P F K P N Y Y R Y \*  
 1861 CAAGGACCAGTCCACCTGAACCACACACTCTAAAGAAAATTTTAAGATAACTTTAT + 1920  
 1921 TTTCTTCTTACTCCTTCTTGTATTTTCTATAATTCTATTCTGTTTTCATC + 1980  
 1981 TCATTATCCAAGTTCTGCAGACCACACAGGAACCTGCTTCATGGCTCTTAGATGAAATA + 2040

FIG 1 (cont)

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GAAGTTCAGGGTCCCTCACTCTAGTCACTAAAGAAGGATTTACTCCCCAGCCCAGAAA  
2041 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2100

GGTGATTCTCTCTTACCATTTCTGGGGACTTAGTCTTAATTAGGTACCTTATTAACA  
2101 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2160

GGAAATGCTAAGGTACCTCTGTGGAACAATCTGCAATGTCTAAATCGCCTTAAAGA  
2161 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2220

GCCCATTCTTAGCTGCTGAAATCAGTGCTTTCACTTCTCAGAGAACAGGGATGGT  
2221 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2280

ACCTACCCGGCAGGTAGGTTAGATGTGGTGGTGCATGTTAATTCCCTTAGAAGTTCCA  
2281 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2340

AGCCCTGTTCTCGTAAAGGTGGTATGTCCAGAGATGTGTATAATGAGCATGG  
2341 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2400

CTTGTTAAGATCAGGAGGCCACTGGATTTATAGTATAGCCCTCCTCCACTCCACCA  
2401 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2460

GACTTGCTCATTTCGAGTTTAACTAGACTACACTCTATTGAGTTAATTGTCC  
2461 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2520

TCTAGGATTTATTCTGTTGTCCAAAAAAAAAAAAAAAAAAAA  
2521 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2563

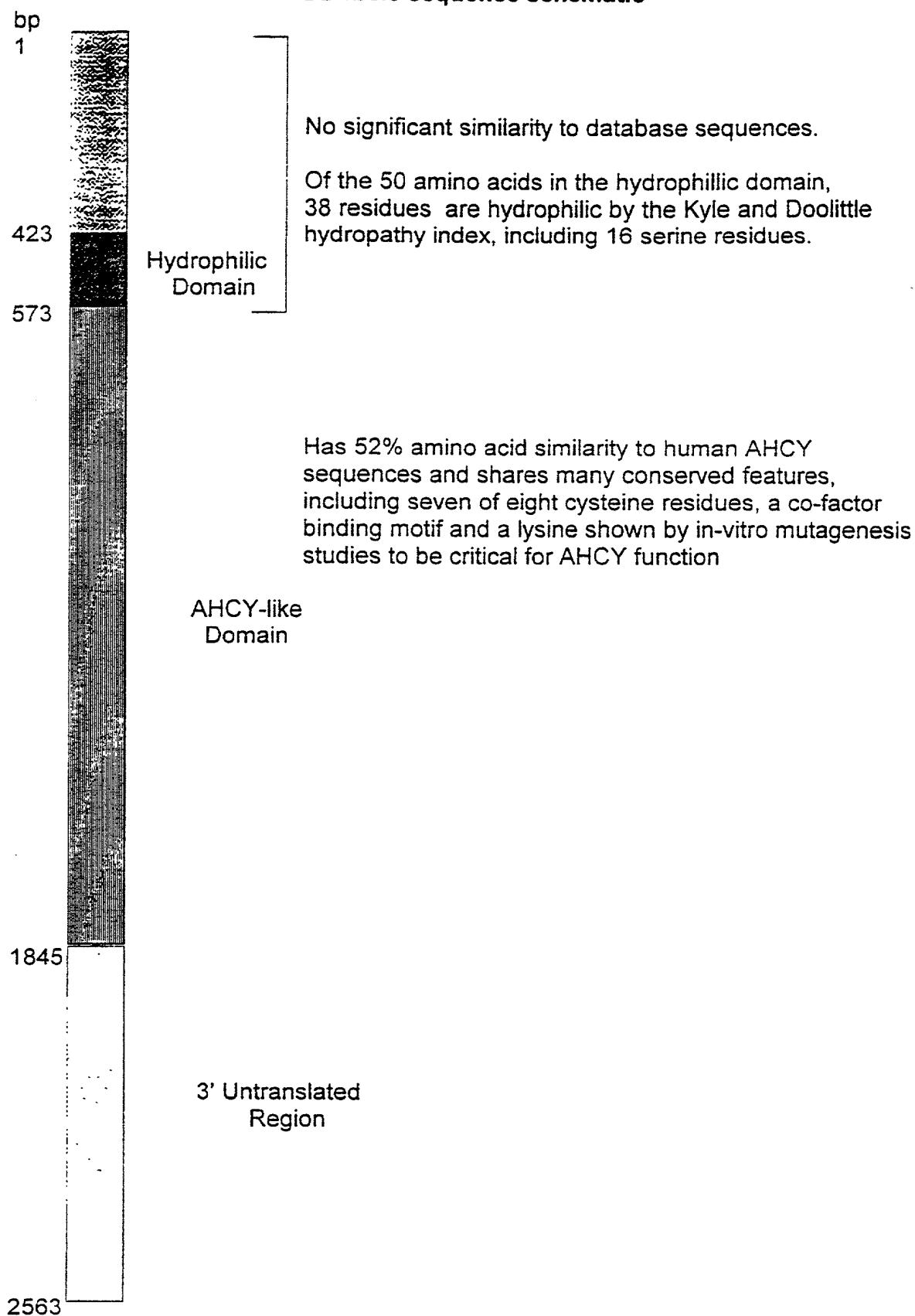
FIG 1 (Cont)

Alignment of DD4b5.3 AHCY-like domain with full-length AHCY amino acid sequences of human (hu), mouse (mu) and drosophila (dr). Noted are conserved features shown to be important for AHCY function



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## DD4b5.3 sequence schematic



## Southern blot analysis of DD4b5.3 RT-PCR results

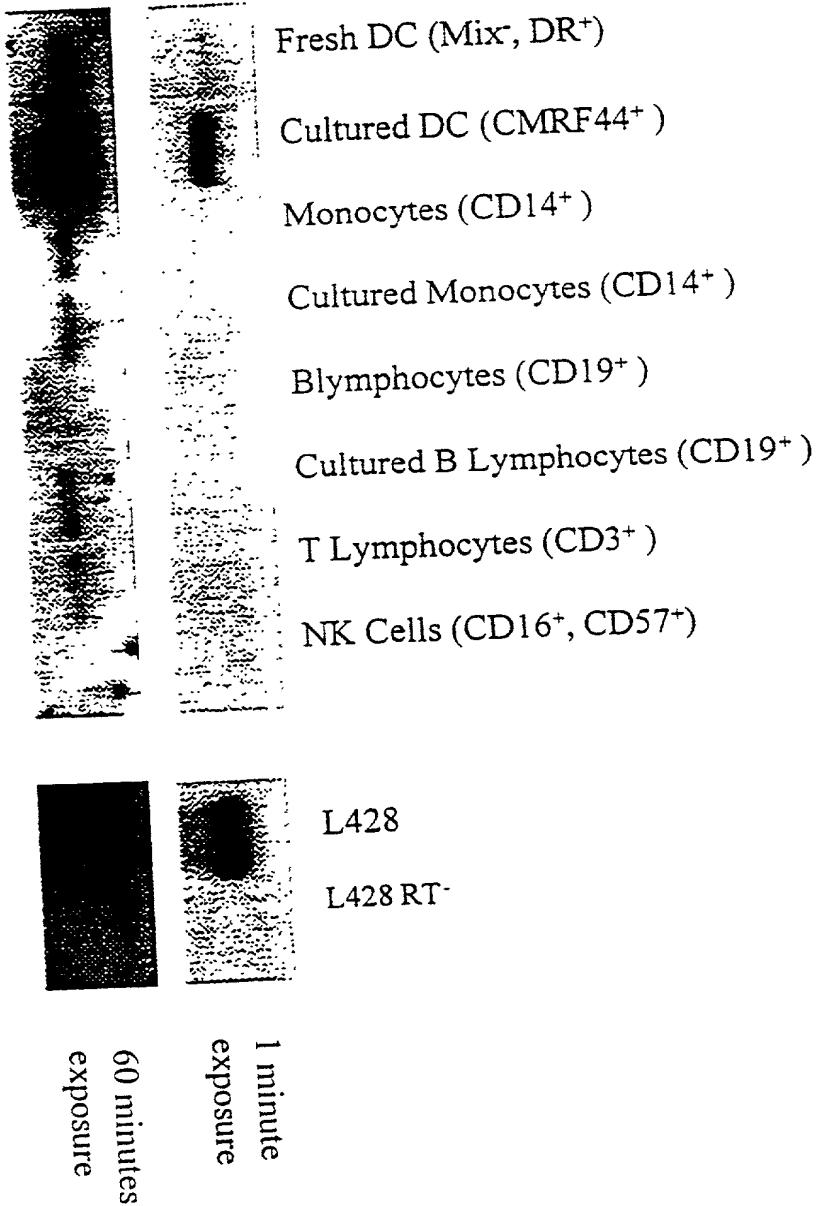


FIG 4

## Expression of DD4b5.3 in DC lineage panel, as assessed by RT-PCR

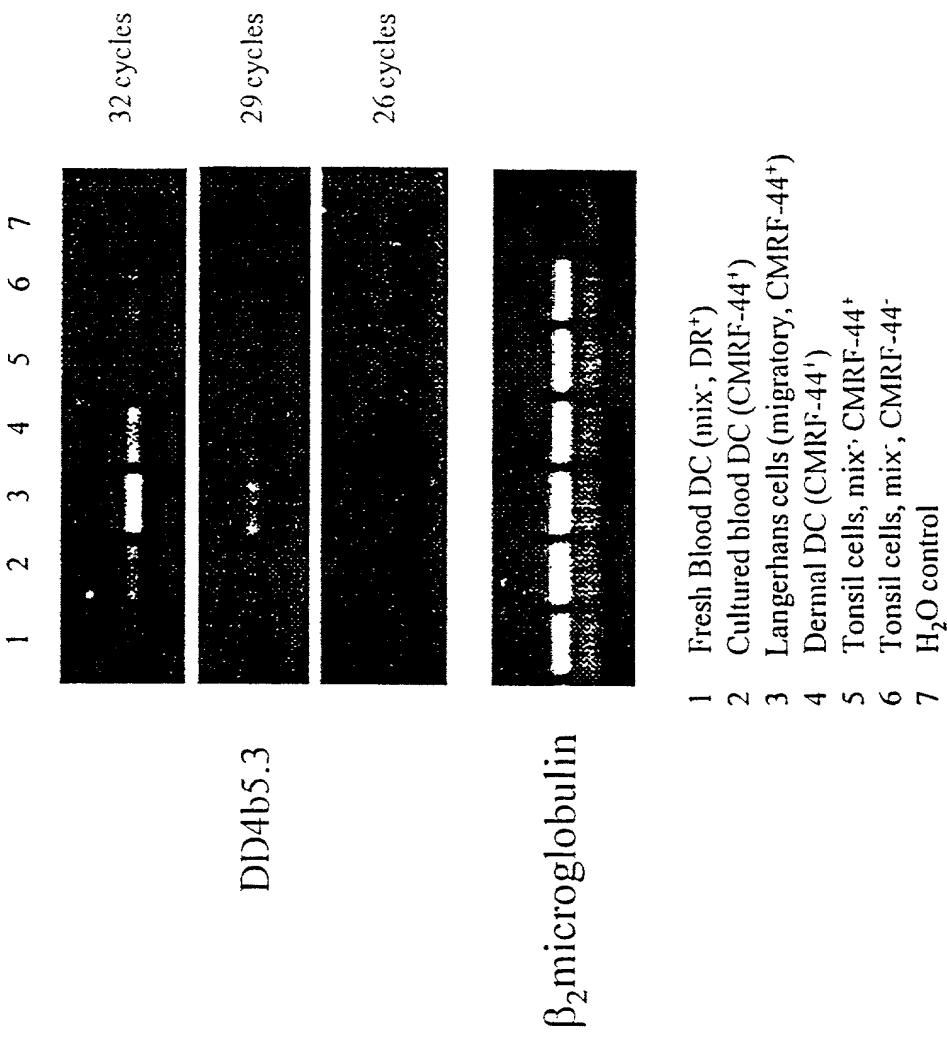


FIG 5

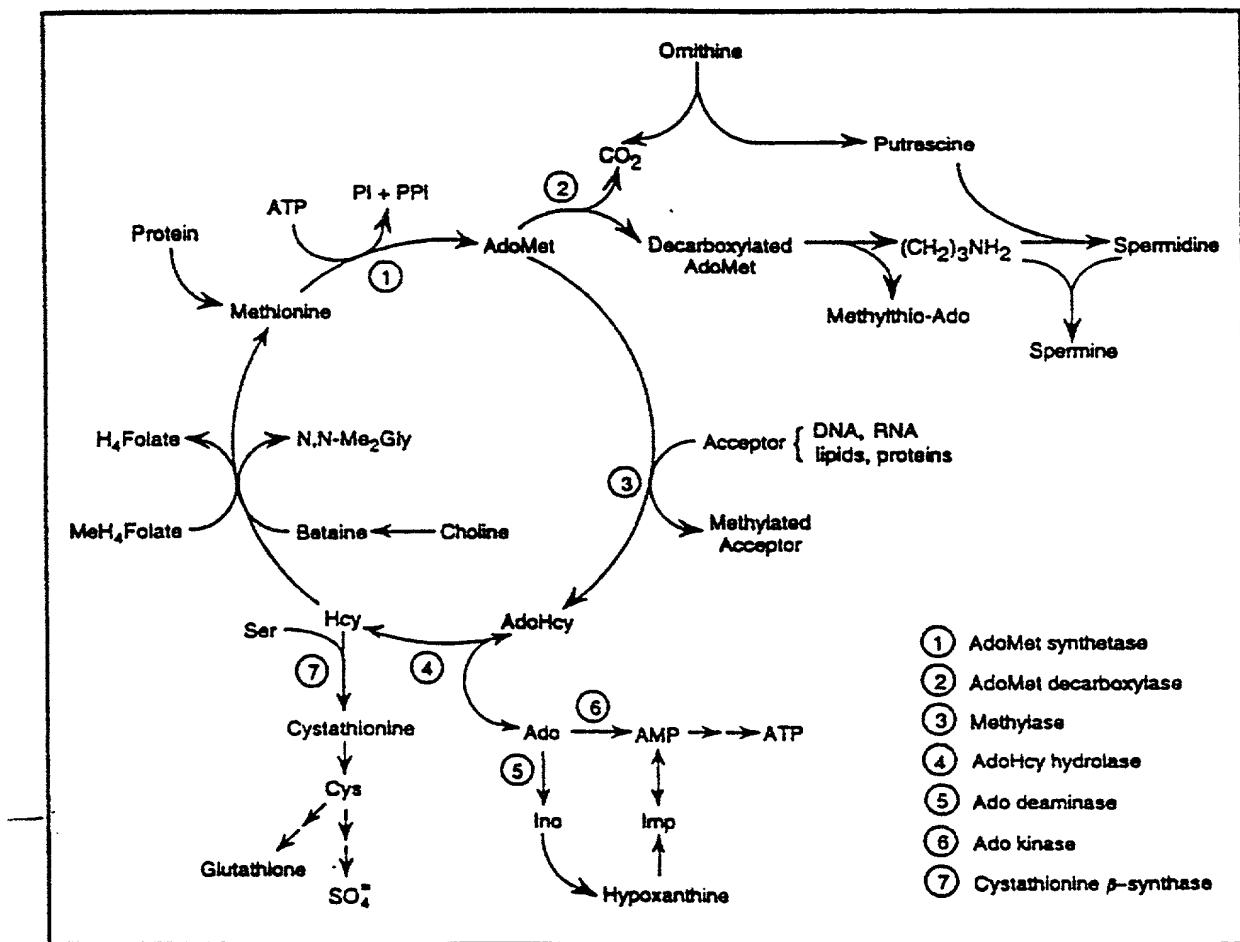


FIG 6

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## RAP-PCR Method

